



SEQUENCE LISTING

#8
RECEIVED
AUG 31 2001
TECH CENTER 1600/2900

<110> Mark Marchionni
Michael Jarpe
Ted Ebendal

<120> METHODS FOR TREATING NEUROLOGICAL
INJURIES AND DISORDERS

<130> 47506 (71095)

<140> 09/756,481

<141> 2001-01-08

<150> PCT/US99/15106

<151> 1999-07-02

<150> 60/091,791

<151> 1998-07-06

<160> 2

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1387

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (218)...(1288)

<400> 1

cccttctcca	gggactctgg	ctgccagcag	ctccgccttt	cagatcaatt	ctcgaccacc	60				
caccttggga	ctgccgcca	gtctgtccct	ctggatcagt	ggggtccaga	cacgccccct	120				
ccaggacctc	aaagcacccc	cgacctaaag	tcaccagccc	actggcccca	gacgcagtgg	180				
gctccgctga	ctctcttgga	cacctcctgg	gaggaaa	atg	ctc	cct	gtc	tgc	cat	235

Met Leu Pro Val Cys His

1

5

cgt	ttt	tgc	gac	cac	ctc	ctc	ctc	ctg	ctc	ttg	ctg	ccc	tcg	acg	acc	283
Arg	Phe	Cys	Asp	His	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Ser	Thr	Thr	
			10					15					20			

ctg	gcc	ccc	gcg	cca	gca	tcc	atg	ggc	ccc	gct	gcc	gcc	ctg	ctc	cag	331
Leu	Ala	Pro	Ala	Pro	Ala	Ser	Met	Gly	Pro	Ala	Ala	Ala	Leu	Leu	Gln	
		25					30				35					

gtt	ctt	ggg	ctt	ccc	gaa	gcg	ccc	cgg	agc	gtc	ccc	aca	cac	cga	cct	379
Val	Leu	Gly	Leu	Pro	Glu	Ala	Pro	Arg	Ser	Val	Pro	Thr	His	Arg	Pro	
		40				45					50					

gtg cct cct gtc atg tgg cgc cta ttc cgt cgc cgt gac ccc cag gag	427
Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp Pro Gln Glu	
55 60 65 70	
gcc aga gtg gga cgc cct ctg cgg cca tgc cac gtg gag gaa cta ggg	475
Ala Arg Val Gly Arg Pro Leu Arg Pro Cys His Val Glu Glu Leu Gly	
75 80 85	
gtc gcc gga aac att gtg cgc cac atc ccc gac agc ggt ctg tcc tcc	523
Val Ala Gly Asn Ile Val Arg His Ile Pro Asp Ser Gly Leu Ser Ser	
90 95 100	
agg ccc gca caa ccc gcc agg acc tcg ggg ctg tgc ccc gag tgg aca	571
Arg Pro Ala Gln Pro Ala Arg Thr Ser Gly Leu Cys Pro Glu Trp Thr	
105 110 115	
gtc gtc ttt gac ctg tcg aat gtg gag ccc aca gag cgc cca aca cgc	619
Val Val Phe Asp Leu Ser Asn Val Glu Pro Thr Glu Arg Pro Thr Arg	
120 125 130	
gcg cgc tta gag ttg cgg ctg gag gct gag tgt gaa gat aca gga ggg	667
Ala Arg Leu Glu Leu Arg Leu Glu Ala Glu Cys Glu Asp Thr Gly Gly	
135 140 145 150	
tgg gag cta agc gtg gca ctg tgg gcc gac gca gag cat cca ggg cct	715
Trp Glu Leu Ser Val Ala Leu Trp Ala Asp Ala Glu His Pro Gly Pro	
155 160 165	
gag ctg ctg cgc gtg ccg gcg cca cca ggg gtg ctc ctg cgc gca gac	763
Glu Leu Leu Arg Val Pro Ala Pro Pro Gly Val Leu Leu Arg Ala Asp	
170 175 180	
cta ctg ggg act gca gta gcc gcc aac gca tca gtg ccc tgt act gtg	811
Leu Leu Gly Thr Ala Val Ala Ala Asn Ala Ser Val Pro Cys Thr Val	
185 190 195	
cgc ctg gcg ctg tca ctg cac cct ggg gcc act gca gcc tgt ggg cgc	859
Arg Leu Ala Leu Ser Leu His Pro Gly Ala Thr Ala Ala Cys Gly Arg	
200 205 210	
ctg gct gag gcc tcc ctg ctg ctg gtg acg ctg gac cca cgc ctg tgt	907
Leu Ala Glu Ala Ser Leu Leu Leu Val Thr Leu Asp Pro Arg Leu Cys	
215 220 225 230	
ccc ttg ccg cga ttg cgg cgc cac acg gag ccc agg gta gaa gtt ggt	955
Pro Leu Pro Arg Leu Arg Arg His Thr Glu Pro Arg Val Glu Val Gly	
235 240 245	
cca gtg ggc act tgt cgt acc cga cgg ttg cat gtg agc ttc cgt gag	1003
Pro Val Gly Thr Cys Arg Thr Arg Arg Leu His Val Ser Phe Arg Glu	
250 255 260	

gtg ggc tgg cac cgt tgg gtg atc gcg ccg cgt ggc ttc cta gcc aac	1051
Val Gly Trp His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn	
265 270 275	
ttc tgc cag ggc acg tgc gca cta ccc gaa acg ctg agg gga ccc ggc	1099
Phe Cys Gln Gly Thr Cys Ala Leu Pro Glu Thr Leu Arg Gly Pro Gly	
280 285 290	
ggg ccg cct gca ctc aac cac gct gtg ctg cgc gcg ctc atg cac gca	1147
Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala	
295 300 305 310	
gct gct ccc acc ccg ggt gca ggc tcg ccc tgc tgc gtg cca gag cgt	1195
Ala Ala Pro Thr Pro Gly Ala Gly Ser Pro Cys Cys Val Pro Glu Arg	
315 320 325	
cta tca ccc atc tcc gtg ctc ttc ttc gac aat agt gac aac gtg gtc	1243
Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val	
330 335 340	
ctg cga cac tac gaa gac atg gtg gtg gat gag tgt ggc tgc cgt	1288
Leu Arg His Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg	
345 350 355	
tgaccacccg ggacaccctt tcagggaccg ccccacgcaa aagcagggac tgtttgttca	1348
tgttttattg gtgacaaaaa gcttaaaaca aatttgact	1387

<210> 2
 <211> 357
 <212> PRT
 <213> Artificial Sequence

<400> 2

Met	Leu	Pro	Val	Cys	His	Arg	Phe	Cys	Asp	His	Leu	Leu	Leu	Leu	Leu
1				5				10					15		
Leu	Leu	Pro	Ser	Thr	Thr	Leu	Ala	Pro	Ala	Pro	Ala	Ser	Met	Gly	Pro
			20				25					30			
Ala	Ala	Ala	Leu	Leu	Gln	Val	Leu	Gly	Leu	Pro	Glu	Ala	Pro	Arg	Ser
		35				40					45				
Val	Pro	Thr	His	Arg	Pro	Val	Pro	Pro	Val	Met	Trp	Arg	Leu	Phe	Arg
	50				55				60						
Arg	Arg	Asp	Pro	Gln	Glu	Ala	Arg	Val	Gly	Arg	Pro	Leu	Arg	Pro	Cys
65				70			75							80	
His	Val	Glu	Glu	Leu	Gly	Val	Ala	Gly	Asn	Ile	Val	Arg	His	Ile	Pro
			85			90							95		
Asp	Ser	Gly	Leu	Ser	Ser	Arg	Pro	Ala	Gln	Pro	Ala	Arg	Thr	Ser	Gly
			100				105					110			
Leu	Cys	Pro	Glu	Trp	Thr	Val	Val	Phe	Asp	Leu	Ser	Asn	Val	Glu	Pro
		115				120						125			
Thr	Glu	Arg	Pro	Thr	Arg	Ala	Arg	Leu	Glu	Leu	Arg	Leu	Glu	Ala	Glu
	130					135					140				

[illegible]